RAW SEQUENCE LISTING
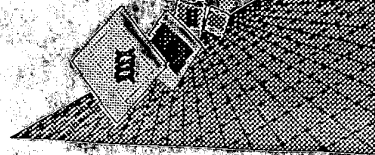# ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: **09/709,905**

Source: **OIPE**

Date Processed by STIC: **3/13/2001**

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

```
RAW SEQUENCE LISTING            DATE: 03/13/2001
PATENT APPLICATION:  US/09/709,905     TIME: 15:05:04

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw
```

```
 4 <110> APPLICANT: Kalyanaraman Ramnarayan
 5         Edward T. Maggio
 6         P. Patrick Hess
 9 <120> TITLE OF INVENTION: Use of Computationally Derived Protein
10         Structures of Genetic Polymorphisms in Pharmacogenomics for
11         Drug Design and Clinical Applications
15 <130> FILE REFERENCE: 24737-1906C
17 <140> CURRENT APPLICATION NUMBER: US/09/709,905
18 <141> CURRENT FILING DATE: 2000-11-10
20 <150> PRIOR APPLICATION NUMBER: 09/438,566
21 <151> PRIOR FILING DATE: 1999-11-10
23 <150> PRIOR APPLICATION NUMBER: 24737-1906B
24 <151> PRIOR FILING DATE: 2000-11-01
26 <160> NUMBER OF SEQ ID NOS: 118
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 6
32 <212> TYPE: PRT
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Modified Hepatitis C Virus NS3 Protease Inhibitor
37         Peptide
40 <221> NAME/KEY: ACETYLATION
41 <222> LOCATION: 1
43 <221> NAME/KEY: MOD_RES
44 <222> LOCATION: 2
45 <223> OTHER INFORMATION: D-glutamic acid
47 <221> NAME/KEY: MOD_RES
48 <222> LOCATION: 5
49 <223> OTHER INFORMATION: beta-cyclohexylalanine
51 <300> PUBLICATION INFORMATION:
52 <301> AUTHORS: Ingallinella, P., Altamura, S., Bianchi, E., Talia
53 <302> TITLE: Potent Peptide Inhibitors Of Human Hepatitis C Vir
54 <303> JOURNAL: Biochemistry
55 <304> VOLUME: 37
56 <305> ISSUE: 25
57 <306> PAGES: 8906-8914
58 <307> DATE: 1998-06-23
60 <400> SEQUENCE: 1
61 Asp Xaa Leu Ile Xaa Cys
62 1               5
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 6
66 <212> TYPE: PRT
67 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Modified Hepatitis C Virus NS3 Protease Inhibitor
```

**Does Not Comply
Corrected Diskette Needed**

```
 71         Peptide
 75 <221> NAME/KEY: ACETYLATION
 76 <222> LOCATION: 1
 78 <221> NAME/KEY: MOD_RES
 79 <222> LOCATION: 5
 80 <223> OTHER INFORMATION: beta-cyclohexylalanine
 82 <300> PUBLICATION INFORMATION:
 83 <301> AUTHORs: Ingallinella, P., Altamura, S., Bianchi, E., Talia
 84 <302> TITLE: Potent Peptide Inhibitors Of Human Hepatitis C Vir
 85 <303> JOURNAL: Biochemistry
 86 <304> VOLUME: 37
 87 <305> ISSUE: 25
 88 <306> PAGES: 8906-8914
 89 <307> DATE: 1998-06-23
 91 <400> SEQUENCE: 2
 92 Asp Glu Leu Ile Xaa Cys
 93 1               5
 95 <210> SEQ ID NO: 3
 96 <211> LENGTH: 1045
 97 <212> TYPE: DNA
 98 <213> ORGANISM: Human Immunodeficiency Virus (HIV)
100 <220> FEATURE:
101 <221> NAME/KEY: CDS
102 <222> LOCATION: (0)..(297)
103 <223> OTHER INFORMATION: Protease
105 <221> NAME/KEY: CDS
106 <222> LOCATION: (298)...(1045)
107 <223> OTHER INFORMATION: Portion of Reverse Transcriptase
109 <400> SEQUENCE: 3
110 cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg     48
111 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
112 1               5                   10                  15
114 ggc caa cta aaa gaa gct yta tta gat aca gga gca gat gat aca gta     96
115 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
116             20                  25                  30
118 tta gaa gaa atg agt tta cca ggg aaa tgg aaa cca aaa atg ata ggg    144
119 Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
120         35                  40                  45
122 gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata ctc ata    192
123 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
124         50                  55                  60
126 gaa atc tgt gga cat aaa gct ata ggc aca gta tta gta gga cct aca    240
127 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
128 65                  70                  75                  80
130 cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act    288
131 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
132                 85                  90                  95
134 tta aat ttg ccc att agt cct att gaa act gta cca gta aaa tta aag    336
135 Leu Asn Leu Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
```

(handwritten annotations:) e (global error)

(1) ← coding begins at first base (global error)

RAW SEQUENCE LISTING   DATE: 03/13/2001
PATENT APPLICATION: US/09/709,905   TIME: 15:05:04

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

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136             100              105               110
138 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa       384
139 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
140         115              120               125
142 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga       432
143 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
144         130              135               140
146 aaa att tca aaa att ggg cct gag aat cca tac aat act cca ata ttt       480
147 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
148 145              150              155               160
150 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc       528
151 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
152         165              170               .175
154 aga gaa ctt aat aag aga aca caa gac ttc tgg gaa gtt caa tta gga       576
155 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
156         180              185               190
158 ata cca cac ccc gca ggg tta aaa cag aaa aaa tca gta aca ata ctg       624
159 Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu
160         195              200               205
162 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa ggc ttc agg       672
163 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg
164         210              215               220
166 aag tat act gca ttt acc ata cct agt aga aat aat gag aca cca ggg       720
167 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly
168 225              230              235               240
170 att aga tat cag tac aac gtg ctc cca cag gga tgg aaa gga tca cca       768
171 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
172         245              250               255
174 gca ata ttt caa agt agc atg aca aga aty tta gag cct ttt aga aaa       816
175 Ala Ile Phe Gln Ser Ser Met Thr Arg Xaa Leu Glu Pro Phe Arg Lys
176         260              265               270
178 caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta       864
179 Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
180         275              280               285
182 gga tct gac tta gaa ata gga cag cat aga gca aaa ata gag gaa ctg       912
183 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
184         290              295               300
186 aga gga cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat       960
187 Arg Gly His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
188 305              310              315               320
190 cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat       1008
191 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
192              325              330               335
194 aaa tgg aca gta cag cct ata aag ttg cca gaa aaa g                     1045
195 Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys
196              340              345
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 1046
201 <212> TYPE: DNA
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            RAW SEQUENCE LISTING                    DATE: 03/13/2001
            PATENT APPLICATION:  US/09/709,905      TIME: 15:05:04

            Input Set : A:\1906cseq.002
            Output Set: N:\CRF3\03132001\I709905.raw

     202 <213> ORGANISM: Human Immunodeficiency Virus (HIV)
     204 <220> FEATURE:
     205 <221> NAME/KEY: CDS  (1)
W--> 206 <222> LOCATION: (0)...(297)
     207 <223> OTHER INFORMATION: HIV Protease
     209 <221> NAME/KEY: CDS
     210 <222> LOCATION: (298)...(1046)
     211 <223> OTHER INFORMATION: Portion of HIV Reverse Transcriptase
     213 <400> SEQUENCE: 4
     214 cct cag atc act ctt tgg caa cga ccc ctt gtc aca ata aag ata gga      48
     215 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
     216 1               5                  10                  15
     218 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
     219 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
     220             20                  25                  30
     222 gtt gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg     144
     223 Val Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
     224         35                  40                  45
     226 gga att gga ggt ttt atc aaa gta aga cag tat gag caa ata gcc gta     192
     227 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile Ala Val
     228     50                  55                  60
     230 gaa aty tgt gga cat aga gct atg ggt aca gta tta gta gga cct aca     240
     231 Glu Xaa Cys Gly His Arg Ala Met Gly Thr Val Leu Val Gly Pro Thr
     232 65                  70                  75                  80
     234 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act     288
     235 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
     236                 85                  90                  95
     238 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag     336
     239 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
     240             100                 105                 110
     242 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa     384
     243 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
     244         115                 120                 125
     246 aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa ggg     432
     247 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
     248     130                 135                 140
     250 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt     480
     251 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
     252 145                 150                 155                 160
     254 gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc     528
     255 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
     256                 165                 170                 175
     258 aga gaa ctt aat aag aga act caa gac ttc tgg gag gtt caa tta gga.     576
     259 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
     260             180                 185                 190
     262 ata cca cat cca gca ggg tta aaa aag aat aaa tca ata aca gta ctg     624
     263 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ile Thr Val Leu
     264             195                 200                 205
     266 gat gtg ggt gat gca tat ttt tca gtt ccc tta tgt gaa gac ttc agg     672
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RAW SEQUENCE LISTING   DATE: 03/13/2001
PATENT APPLICATION: US/09/709,905   TIME: 15:05:04

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

```
267 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Cys Glu Asp Phe Arg
268     210             215             220
270 aag tat act gca ttt acc ata cct agt gta aac aat gag act cca ggg      720
271 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
272 225             230             235             240
274 att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga ttc acc      768
275 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Phe Thr
276             245             250             255
278 agc ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa      816
279 Ser Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
280             260             265             270
282 caa aat cca gag ata gtt atc tat caa tac atg gat gat ttg tat gta      864
283 Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
284             275             280             285
286 gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg      912
287 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
288     290             295             300
290 aga caa tat ctg tgg aag tgg gga ttt tgc aca cca gaa caa aar cat      960
291 Arg Gln Tyr Leu Trp Lys Trp Gly Phe Cys Thr Pro Glu Gln Lys His
292 305             310             315             320
294 cag aaa gaa cct cct ttc ctt tgg atg ggt tat gaa ctc cat ccc gat      1008
295 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
296             325             330             335
298 aaa tgg aca gta caa cct ata gtg ctg cca gac aaa ga                   1046
299 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys
300             340             345
303 <210> SEQ ID NO: 5
304 <211> LENGTH: 1104
305 <212> TYPE: DNA
306 <213> ORGANISM: Human Immunodeficiency Virus (HIV)
308 <220> FEATURE:
309 <221> NAME/KEY: CDS
310 <222> LOCATION: (0)...(297)
311 <223> OTHER INFORMATION: HIV Protease
313 <221> NAME/KEY: CDS
314 <222> LOCATION: (298)...(1104)
315 <223> OTHER INFORMATION: Portion of HIV Reverse Transcriptase
317 <400> SEQUENCE: 5
318 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag rta ggg       48
319 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Xaa Gly
320 1               5               10              15
322 ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca ata       96
323 Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile
324             20              25              30
326 ata gaa gac ata act ttg cca gga aga tgg aca cca aaa atg ata ggg      144
327 Ile Glu Asp Ile Thr Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly
328     35              40              45
330 gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata      192
331 Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
```

Annotations (handwritten): *e*, *(1)*, W--> near 310, *(0)*, near 314, near 319 "W/L", *OK* marks.

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

FYI:

Please Note:
Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least ne n or Xaa.

```
VERIFICATION SUMMARY                          DATE: 03/13/2001
PATENT APPLICATION:  US/09/709,905            TIME: 15:05:05

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw
```

```
L:17 M:270 C: Current Application Number differs, Replaced Current Application Number
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:102 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:3, CDS LOCATION: (0)...(297)
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:206 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: (0)...(297)
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:310 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION: (0)...(297)
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:418 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:6, CDS LOCATION: (0)...(297)
L:530 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (0)...(297)
L:546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:642 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:8, CDS LOCATION: (0)...(297)
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:754 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:9, CDS LOCATION: (0)...(297)
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:866 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:10, CDS LOCATION: (0)...(297)
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:978 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION: (0)...(297)
L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1090 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:12, CDS LOCATION: (0)...(297)
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1202 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:13, CDS LOCATION: (0)...(297)
L:1211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1314 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:14, CDS LOCATION: (0)...(297)
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1426 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:15, CDS LOCATION: (0)...(297)
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VERIFICATION SUMMARY   DATE: 03/13/2001
PATENT APPLICATION: US/09/709,905   TIME: 15:05:05

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

```
L:1443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1538 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:16, CDS LOCATION: (0)...(297)
L:1579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1650 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:17, CDS LOCATION: (0)...(297)
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1762 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:18, CDS LOCATION: (0)...(297)
L:1783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1874 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:19, CDS LOCATION: (0)...(297)
L:1986 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:20, CDS LOCATION: (0)...(297)
L:2098 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:21, CDS LOCATION: (0)...(297)
L:2210 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:22, CDS LOCATION: (0)...(297)
L:2322 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:23, CDS LOCATION: (0)...(297)
L:2434 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:24, CDS LOCATION: (0)...(297)
L:2546 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:25, CDS LOCATION: (0)...(297)
L:2658 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:26, CDS LOCATION: (0)...(297)
L:2770 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:27, CDS LOCATION: (0)...(297)
L:2774 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:27, CDS LOCATION: (298)...(1116)
L:2882 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:28, CDS LOCATION: (0)...(297)
L:2994 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:29, CDS LOCATION: (0)...(297)
L:3106 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:30, CDS LOCATION: (0)...(297)
L:3218 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:31, CDS LOCATION: (0)...(297)
L:3330 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:32, CDS LOCATION: (0)...(297)
L:3442 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:33, CDS LOCATION: (0)...(297)
L:3554 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:34, CDS LOCATION: (0)...(297)
L:3666 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:35, CDS LOCATION: (0)...(297)
L:3778 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:36, CDS LOCATION: (0)...(297)
L:3890 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:37, CDS LOCATION: (0)...(297)
L:4002 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, CDS LOCATION: (0)...(297)
L:4114 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:39, CDS LOCATION: (0)...(297)
L:4226 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:40, CDS LOCATION: (0)...(297)
L:4338 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:41, CDS LOCATION: (0)...(297)
L:4446 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:42, CDS LOCATION: (0)...(297)
L:4550 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:43, CDS LOCATION: (0)...(297)
L:4658 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:44, CDS LOCATION: (0)...(297)
L:4770 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:45, CDS LOCATION: (0)...(297)
L:4882 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:46, CDS LOCATION: (0)...(297)
L:4994 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:47, CDS LOCATION: (0)...(297)
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VERIFICATION SUMMARY   DATE: 03/13/2001
PATENT APPLICATION: US/09/709,905   TIME: 15:05:05

Input Set : A:\1906cseq.002
Output Set: N:\CRF3\03132001\I709905.raw

L:5106 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:48, CDS LOCATION: (0)...(297)
L:5218 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:49, CDS LOCATION: (0)...(297)
L:5330 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:50, CDS LOCATION: (0)...(297)
L:5442 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:51, CDS LOCATION: (0)...(297)